In the Claims

Please amend and add the following claims according to the following listing of claims under 37 CFR 1.121.

Listing of Claims under 37 CFR 1.121:
1-90 (CANCELED)

91. (NEW): A composition, comprising: one or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers, wherein the group of covering markers is chosen so that a CL-F region is systematically covered by the covering markers, the covering markers and the CL-F region being for a species of creatures, the CL-F region being a collection of one or more points on a two-dimensional CL-F map that is similar to an x-y graph, the CL-F map having the two orthogonal dimensions of chromosomal location (CL) and least common allele frequency (F), wherein the group of covering markers comprises thousands of bi-allelic markers, wherein there are covering markers with least common allele frequencies less than or equal to 0.3.

92. (NEW): A composition as in claim 91, wherein each oligonucleotide in the set is a type (1) complementary oligoncucleotide or wherein each oligonucleotide in the set is a type (2) complementary oligonucleotide, wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to about D_{CL} or the equivalent thereof and y is less than or equal to about 0.2, D_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

93. (NEW): A composition as in claim 92, wherein x is less than about D_{CL}, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific and each covering marker is an SNP.

94. (NEW): A composition as in claim 91, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific and each covering marker is an SNP, wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein [x, y] is a two-dimensional distance, wherein N is an integer greater than or equal to 1, wherein y is less than or equal to about 0.2 and x is less than or equal to about 10 to 12 cM.

95. (NEW): A composition as in claim 94, wherein y is less than or equal to 0.2.

96. (NEW): A composition as in claim 95, wherein there are covering markers with least common allele frequencies less than 0.2.

97. (NEW): A composition as in claim 95, wherein there are covering markers with least common allele frequencies less than or equal to 0.1.

98. (NEW): A composition as in claim 94, wherein x is less than or equal to about 1 million base pairs.

99. (NEW): A composition as in claim 98, wherein there are covering markers with least common allele frequencies less than 0.2.

100. (NEW): A composition as in claim 98, wherein there are covering markers with least common allele frequencies less than or equal to 0.1.

101. (NEW): A composition as in claim 95, wherein x is less than or equal to 250,000 base pairs.

102. (NEW): A composition as in claim 101, wherein there are covering markers with least common allele frequencies less than 0.2.

103. (NEW): A composition as in claim 101, wherein there are covering markers with least common allele frequencies less than or equal to 0.1.

104. (NEW): A composition as in claim 95, wherein the CL-F region is a segment-subrange, wherein the segment of the segment-subrange is a segment of a chromosome and the length of the chromosome segment is equal to the length of the chromosome and wherein the subrange of the segment-subrange is the subrange 0 to 0.5, whereby the segment-subrange is a rectangular CL-F region that is bounded by the segment and the subrange.

105. (NEW): A composition as in claim 104, wherein x is less than or equal to 250,000 base pairs.

106. (NEW): A composition as in claim 105, wherein N is greater than 2, the species is human being and the chromosome is any one of human chromosomes 1-6.

107. (NEW): A composition as in claim 105, wherein N is greater than 2, y is 0.1, the species is human being and the chromosome is any one of human chromosomes 1-13.

108. (NEW): A composition as in claim 95, wherein the CL-F region is a segment-subrange, wherein the segment of the segment-subrange is a segment of a chromosome and the length of the chromosome segment is equal to the length of the chromosome and wherein the subrange of the segment-subrange is the subrange 0 to less than 0.1, whereby the segment-subrange is a rectangular CL-F region that is bounded by the segment and the subrange.

109. (NEW): A composition as in claim 108, wherein x is less than or equal to 250,000 base pairs.

110. (NEW): A composition as in claim 91, wherein the CL-F region is for a species and a population, wherein the species is human being, wherein the population is a population as in the field of population genetics, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific and each covering marker is an SNP, wherein a chromosome is completely covered by the chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein each covering marker belongs to a subset of covering markers, wherein there is more than one marker in each subset, whereby there are two or more markers in each subset, wherein the markers in each subset have approximately the same least common allele frequencies, wherein the difference between the least common allele frequencies of any two markers in each subset does not exceed 0.15, wherein the markers in each subset are located within one segment and within each segment there are five subsets, or more or less than five subsets of covering markers, wherein the approximate least common allele frequencies of the markers in each subset are spaced approximately evenly over a least common allele frequency subrange.

111. (NEW): A composition as in claim 93, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides; or wherein the apparatus comprises a glass slide and copies of the set of oligonucleotides are attached to the glass slide; or wherein the apparatus comprises a silicon chip and copies of the set of oligonucleotides are attached to the silicon chip.

112. (NEW): A composition as in claim 94, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.

113. (NEW): A composition as in claim 95, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.

114. (NEW): A composition as in claim 96, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
115. (NEW): A composition as in claim 101, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
116. (NEW): A composition as in claim 102, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
117. (NEW): A composition as in claim 103, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
118. (NEW): A composition as in claim 104, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
119. (NEW): A composition as in claim 105, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
120. (NEW): A composition as in claim 106, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
121. (NEW): A composition as in claim 107, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
122. (NEW): A composition as in claim 108, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
123. (NEW): A composition as in claim 109, wherein an apparatus comprises copies of the set of oligonucleotides, wherein the apparatus comprises a high-density oligonucleotide array and the array comprises copies of the set of oligonucleotides.
124. (NEW): A composition as in claim 93, wherein the species is human being.

125. (NEW): A composition as in claim 94, wherein the species is human being.
126. (NEW): A composition as in claim 95, wherein the species is human being.
127. (NEW): A composition as in claim 96, wherein the species is human being.
128. (NEW): A composition as in claim 97, wherein the species is human being.
129. (NEW): A composition as in claim 101, wherein the species is human being.
130. (NEW): A composition as in claim 105, wherein the species is human being.
131. (NEW): A composition as in claim 108, wherein the species is human being.
132. (NEW): A composition as in claim 109, wherein the species is human being.
133. (NEW): A composition as in claim 113, wherein the species is human being.
134. (NEW): A composition as in claim 114, wherein the species is human being.
135. (NEW): A composition as in claim 116, wherein the species is human being.
136. (NEW): A composition as in claim 118, wherein the species is human being.
137. (NEW): A composition as in claim 119, wherein the species is human being.
138. (NEW): A composition as in claim 122, wherein the species is human being.
139. (NEW): A composition as in claim 123, wherein the species is human being.
140. (NEW): A process for identifying one or more bi-allelic markers linked to a bi-allelic trait-causing polymorphism in a species of creatures, comprising the acts of:

a) choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of one or more points on a two-dimensional map, the two-dimensional map having the two dimensions of chromosomal location and least common allele frequency;

b) choosing a statistical linkage test based on allelic association for each covering marker;

c) choosing a sample of individuals for each covering marker;

d) obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the trait for each individual in the sample chosen for each covering marker;

e) calculating evidence for linkage between each covering marker and the trait-causing polymorphism using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the trait for each individual in the sample chosen for each covering marker obtained in d); and

f) identifying those covering markers as linked to the trait-causing polymorphism which show evidence for linkage based on the calculations of e).

141. (NEW): A process as in claim 140, wherein the CL-F region is for a species, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein x is less than or equal to about D_{CL} or the equivalent thereof and y is less than or equal to about 0.2, D_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, wherein x is short enough that it is possible for polymorphisms within the chromosomal location distance x of each other to be in linkage disequilibrium, N is an integer greater than or equal to 1.

142. (NEW): A process as in claim 141, wherein the CL-F region is a segment-subrange, wherein the width of the subrange of the segment-subrange is less than 0.5 and whereby the segment of the segment-subrange is a chromosome segment and the length of the chromosome segment is less than or equal to the length of the chromosome.

143. (NEW): A process as in claim 141, wherein the process uses thousands of bi-allelic covering markers.

144. (NEW): A process for obtaining genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, each individual in the sample being a member of the same species, comprising:

a) determining information on the presence or absence of each allele of each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, a CL-F region being systematically covered by the two or more bi-allelic covering markers, the CL-F region being a collection of one or more CL-F points on a two-dimensional map, the two-dimensional map having the two dimensions of chromosomal location and least common allele frequency; and

b) transforming the information of step a) into genotype data/sample allele frequency data for each marker of the group.

145. (NEW): A process as in claim 144, wherein the genotype data/sample allele frequency data is genotype data or sample allele frequency data, wherein the CL-F region is for a species, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein x is less than or equal to about D_{CL} or the equivalent thereof and y is less than or equal to about 0.2, D_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, wherein x is short enough that it is possible for polymorphisms within the chromosomal location distance x of each other to be in linkage disequilibrium, N is an integer greater than or equal to 1.

146. (NEW): A process as in claim 145, wherein there are thousands of covering markers.

147. (NEW): A process as in claim 146, wherein the species is not human being.

148. (NEW): A process as in claim 145, wherein there are thousands of covering markers or the density of covering markers is at least thousands per chromosome and wherein the species is a paleospecies, a species hybrid , an agamospecies, an ecosystem species or a plant species.

149. (NEW): An apparatus for obtaining genotype data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals, each individual being a member of a species, wherein the group of covering markers systematically cover a CL-F region, the CL-F region being a collection of one or more CL-F points, wherein the apparatus is a high-density array of oligonucleotides, a nylon membrane with sequence-specific oligonucleotides bound to the membrane, or is oligonucleotides bound to a glass slide or a silicon chip, wherein copies of a set of oligonucleotides that is complementary to the group of two or more bi-allelic covering markers are attached to the apparatus.

150. (NEW): An apparatus as in claim 149, wherein the CL-F region is for a species, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein x is less than or equal to about D_{CL} or the equivalent thereof and y is less than or equal to about 0.2, D_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, wherein x is short enough that it is possible for polymorphisms within the chromosomal location distance x of each other to be in linkage disequilibrium, N is an integer greater than or equal to 1.

151. (NEW): An apparatus as in claim 150, wherein the apparatus is a high-density array of oligonucleotides or the apparatus is oligonucleotides bound to a glass slide or a silicon chip, wherein each covering marker is an exact, true bi-allelic marker.

152. (NEW): An apparatus as in claim 151, wherein thousands of covering markers are from one chromosome.

153. (NEW): An apparatus as in claim 152, wherein the species is not human being.

154. (NEW): An apparatus as in claim 153, wherein there are thousands of covering markers or the density of covering markers is at least thousands per chromosome and wherein the species is not human being and the species is a paleospecies, a species hybrid , an agamospecies, an ecosystem species or a plant species.

155. (NEW): An apparatus as in claim 153, wherein thousands of covering markers are from one chromosome.

156. (NEW): An apparatus as in claim 154, wherein the density of covering markers is at least thousands per chromosome.

157. (NEW): An apparatus as in claim 151, wherein the CL-F region is a segment-subrange, wherein the width of the subrange of the segment-subrange is less than 0.5 and whereby the segment of the segment-subrange is a chromosome segment and the length of the chromosome segment is less than or equal to the length of the chromosome, wherein thousands of covering markers are from the chromosome.

158. (NEW): A process to obtain genotype data/sample allele frequency data, comprising:

obtaining genotype data/sample allele frequency data for each of two or more bi-allelic covering markers, wherein the covering markers systematically cover a CL-F region.

159. (NEW): A process to obtain genotype data/sample allele frequency data, comprising:

obtaining genotype data/sample allele frequency data for each of two or more bi-allelic covering markers, wherein the covering markers systematically cover a CL-F region, wherein the CL-F region is N covered to within [x, y] by the two or more bi-allelic covering markers, wherein x is less than or equal to about D_{CL} or the equivalent thereof and y is less than or equal to about 0.2, D_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, wherein x is short enough that it is possible for polymorphisms within the chromosomal location distance x of each other to be in linkage disequilibrium, N is an integer greater than or equal to 1.

160. (NEW): A process as in claim 159, wherein x is 12 cM and y is 0.2.

161. (NEW): A process as in claim 160, wherein the data is genotype data.

162. (NEW): A process as in claim 160, wherein there are thousands of covering markers.

163. (NEW): A process as in claim 161, wherein there are thousands of covering markers.

164. (NEW): A process as in claim 161, wherein thousands of covering markers are from one chromosome.

165. (NEW): A process for identifying one or more bi-allelic markers linked to a bi-allelic trait-causing polymorphism in a species of creatures, comprising the acts of:

a) choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of one or more points on a two-dimensional map, the two-dimensional map having the two dimensions of chromosomal location and least common allele frequency;

b) choosing a statistical linkage test based on allelic association for each covering marker;

c) choosing a sample of individuals for each covering marker;

d) obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the trait for each individual in the sample chosen for each covering marker;

e) calculating evidence for linkage between each covering marker and the trait-causing polymorphism using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the trait for each individual in the sample chosen for each covering marker obtained in d); and

f) localizing the trait-causing polymorphism to the chromosomal location-least common allele frequency (CL-F) location of one or more markers that show evidence for linkage based on the calculations of act e), wherein the localizing uses a technique or techniques that detects gradients, wherein the detection technique or techniques uses a gradient along the allele frequency dimension.

166. (NEW): A process as in claim 165, wherein the group of two or more covering markers is not an essentially one-dimensional panel of markers for a linkage study, wherein the essentially one-dimensional panel is a panel not based on using similarity of marker allele frequency and possible trait-causing polymorphism allele frequency to increase the power of an association-based linkage test to detect evidence for linkage.